==========

Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=4; day=19; hr=16; min=4; sec=12; ms=154;]

==========

****

Reviewer Comments:

<210> 41

<211> 20

<212> DNA

<213> Synthetic reverse oligonucleotide primer HOM R2

<400> 41

gggcgattag ccattgatac

20

Numeric Identifier <213> can only be one of three choices, “Scientific name, i.e. Genus/species, Unknown or Artificial Sequence.” For all sequences using “Unknown or Artificial sequence”, for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. Suggest using “Artificial sequence” for numeric identifier <213> and “Synthetic reverse oligonucleotide primer HOM R2” for numeric identifier <223> in the mandatory feature. Please check for similar errors and make all necessary changes.

****

Validated By CRFValidator v 1.0.3

Application No: 10562191 Version No: 2.0

Input Set:

Output Set:

Started: 2010-04-14 16:37:33.107
Finished: 2010-04-14 16:37:43.950
Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 843 ms
Total Warnings: 44
Total Errors: 0
No. of SeqIDs Defined: 107
Actual SeqID Count: 107

Error code		Error Description
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W	402	Undefined organism found in <213> in SEQ ID (17)
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W	402	Undefined organism found in <213> in SEQ ID (31)
W	402	Undefined organism found in <213> in SEQ ID (36)
W	213	Artificial or Unknown found in <213> in SEQ ID (39)
W	213	Artificial or Unknown found in <213> in SEQ ID (40)
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W	213	Artificial or Unknown found in <213> in SEQ ID (42)
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W	213	Artificial or Unknown found in <213> in SEQ ID (45)
W	213	Artificial or Unknown found in <213> in SEQ ID (46)
W	213	Artificial or Unknown found in <213> in SEQ ID (47)
W	213	Artificial or Unknown found in <213> in SEQ ID (48)
W	213	Artificial or Unknown found in <213> in SEQ ID (49)
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Input Set:

Output Set:

Started: 2010-04-14 16:37:33.107
Finished: 2010-04-14 16:37:43.950
Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 843 ms
Total Warnings: 44
Total Errors: 0
No. of SeqIDs Defined: 107
Actual SeqID Count: 107

Error code		Error Description
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W	402	Undefined organism found in <213> in SEQ ID (53)
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W	402	Undefined organism found in <213> in SEQ ID (65)
W	402	Undefined organism found in <213> in SEQ ID (72)
W	402	Undefined organism found in <213> in SEQ ID (78) This error has occured more than 20 times, will not be displayed
W	213	Artificial or Unknown found in <213> in SEQ ID (106)

SEQUENCE LISTING

<110> MASIGNANI, Vega
ARICO, Maria Beatrice

<120> VIRULENCE-ASSOCIATED ADHESINS

<130> 2300-20667

<140> 10562191
<141> 2010-04-14

<150> PCT/IB2004/002351
<151> 2004-06-25

<150> GB 0315022.4
<151> 2003-06-26

<160> 107

<170> PatentIn version 3.5

<210> 1
<211> 223
<212> PRT
<213> Haemophilus aegyptius

<400> 1

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Gly Thr Thr Val Ser Asn Tyr Ala Leu Ala Gln Ala Gln Ala Gln Ala
            20                  25                  30


Gln Val Lys Lys Asp Glu Leu Ser Glu Leu Lys Lys Gln Val Lys Glu
        35                  40                  45


Met Asp Ala Ala Ile Asp Gly Ile Leu Asp Asp Asn Ile Ala Tyr Glu
    50                  55                  60


Ala Glu Val Asp Ala Lys Leu Asp Gln His Ser Ala Ala Leu Gly Arg
65                  70                  75                  80


His Thr Asn Arg Leu Asn Asn Leu Lys Thr Ile Ala Glu Lys Ala Lys
                85                  90                  95


Gly Asp Ser Ser Glu Ala Leu Asp Lys Ile Glu Ala Leu Glu Glu Gln
            100                 105                 110
```

```
Asn Asp Glu Phe Leu Ala Asp Ile Thr Ala Leu Glu Glu Gly Val Asp
        115                 120                 125

Gly Leu Asp Asp Asp Ile Ala Gly Ile Gln Asp Asn Ile Ser Asp Ile
    130                 135                 140

Glu Asp Asp Ile Asn Gln Asn Ser Ala Asp Ile Ala Thr Asn Thr Ala
145                 150                 155                 160

Ala Ile Ala Thr His Thr Gln Arg Leu Asp Asn Leu Asp Asn Arg Val
                165                 170                 175

Asn Asn Leu Asn Lys Asp Leu Lys Arg Gly Leu Ala Ala Gln Ala Ala
            180                 185                 190

Leu Asn Gly Leu Phe Gln Pro Tyr Asn Val Gly Lys Leu Asn Leu Thr
        195                 200                 205

Ala Ala Val Gly Gly Tyr Lys Ser Gln Thr Ala Val Ala Val Gly
    210                 215                 220
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<210> 2
<211> 338
<212> PRT
<213> Escherichia coli

<400> 2

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Met Lys Thr Val Asn Val Ala Leu Leu Ala Leu Ile Ile Ser Ala Thr
1               5                   10                  15

Ser Ser Pro Val Val Leu Ala Gly Asp Thr Ile Glu Ala Ala Ala Thr
            20                  25                  30

Glu Leu Ser Ala Ile Asn Ser Gly Met Ser Gln Ser Glu Ile Glu Gln
        35                  40                  45

Lys Ile Thr Arg Phe Leu Glu Arg Thr Asp Asn Ser Pro Ala Ala Tyr
    50                  55                  60

Thr Tyr Leu Thr Glu His His Tyr Ile Pro Ser Glu Thr Pro Asp Thr
65                  70                  75                  80

Thr Gln Thr Pro Thr Val Gln Thr Asp Pro Asp Ala Gly Gln Lys Thr
```

```
                85                  90                  95

Val Ala Ala Thr Gly Asp Val Gln Thr Thr Ala Arg Tyr Gln Ser Met
            100                 105                 110

Ile Asn Ala Arg Gln Ser Ala Val Thr Asp Ala Gln Gln Thr Gln Ile
        115                 120                 125

Thr Glu Gln Gln Ala Gln Ile Val Ala Thr Gln Lys Thr Leu Ala Ala
    130                 135                 140

Thr Gly Asp Thr Gln Asn Thr Ala His Tyr Gln Glu Met Ile Asn Ala
145                 150                 155                 160

Arg Leu Ala Ala Gln Asn Glu Ala Asn Gln Arg Thr Ala Thr Glu Gln
                165                 170                 175

Gly Gln Lys Met Asn Ala Leu Thr Thr Asp Val Ala Val Gln Gln Gln
            180                 185                 190

Asn Glu Arg Thr Gln Tyr Asp Lys Gln Met Gln Ser Leu Ala Gln Glu
        195                 200                 205

Ser Ala Gln Ala His Glu Gln Ile Asp Ser Leu Ser Gln Asp Val Thr
    210                 215                 220

Gln Thr His Gln Gln Leu Thr Asn Thr Gln Lys Arg Val Ala Asp Asn
225                 230                 235                 240

Ser Gln Gln Ile Asn Thr Leu Asn Asn His Phe Ser Ser Leu Lys Asn
                245                 250                 255

Glu Val Asp Asp Asn Arg Lys Glu Ala Asn Ala Gly Thr Ala Ser Ala
            260                 265                 270

Ile Ala Ile Ala Ser Gln Pro Gln Val Lys Thr Gly Asp Val Met Met
        275                 280                 285

Val Ser Ala Gly Ala Gly Thr Phe Asn Gly Glu Ser Ala Val Ser Val
    290                 295                 300

Gly Thr Ser Phe Asn Ala Gly Thr His Thr Val Leu Lys Ala Gly Ile
305                 310                 315                 320
```

Ser Ala Asp Thr Gln Ser Asp Phe Gly Ala Gly Val Gly Val Gly Tyr
325 330 335

Ser Phe

<210> 3
<211> 1588
<212> PRT
<213> Escherichia coli

<400> 3

Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Asn Tyr
1 5 10 15

Thr Val Thr Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
20 25 30

Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Met Leu Ser Ser
35 40 45

Phe Gly Ala Leu Ala Asn Ala Gly Asn Asp Asn Gly Gln Gly Val Asp
50 55 60

Tyr Gly Ser Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly
65 70 75 80

Ala Lys Ala Asn Thr Phe Met Asn Thr Ser Gly Ser Ser Thr Ala Val
85 90 95

Gly Tyr Asp Ala Ile Ala Glu Gly Gln Tyr Ser Ser Ala Ile Gly Ser
100 105 110

Lys Thr His Ala Ile Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala
115 120 125

Ile Ser Glu Gly Asp Arg Ser Ile Ala Leu Gly Ala Ser Ser Tyr Ser
130 135 140

Leu Gly Gln Tyr Ser Met Ala Leu Gly Arg Tyr Ser Lys Ala Leu Gly
145 150 155 160

```
Lys Leu Ser Ile Ala Met Gly Asp Ser Ser Lys Ala Glu Gly Ala Asn
                165                 170                 175

Ala Ile Ala Leu Gly Asn Ala Thr Lys Ala Thr Glu Ile Met Ser Ile
            180                 185                 190

Ala Leu Gly Asp Thr Ala Asn Ala Ser Lys Ala Tyr Ser Met Ala Leu
        195                 200                 205

Gly Ala Ser Ser Val Ala Ser Glu Glu Asn Ala Ile Ala Ile Gly Ala
    210                 215                 220

Glu Thr Glu Ala Ala Glu Asn Ala Thr Ala Ile Gly Asn Asn Ala Lys
225                 230                 235                 240

Ala Lys Gly Thr Asn Ser Met Ala Met Gly Phe Gly Ser Leu Ala Asp
                245                 250                 255

Lys Val Asn Thr Ile Ala Leu Gly Asn Gly Ser Gln Ala Leu Ala Asp
            260                 265                 270

Asn Ala Ile Ala Ile Gly Gln Gly Asn Lys Ala Asp Gly Val Asp Ala
        275                 280                 285

Ile Ala Leu Gly Asn Gly Ser Gln Ser Arg Gly Leu Asn Thr Ile Ala
    290                 295                 300

Leu Gly Thr Ala Ser Asn Ala Thr Gly Asp Lys Ser Leu Ala Leu Gly
305                 310                 315                 320

Ser Asn Ser Ser Ala Asn Gly Ile Asn Ser Val Ala Leu Gly Ala Asp
                325                 330                 335

Ser Ile Ala Asp Leu Asp Asn Thr Val Ser Val Gly Asn Ser Ser Leu
            340                 345                 350

Lys Arg Lys Ile Val Asn Val Lys Asn Gly Ala Ile Lys Ser Asp Ser
        355                 360                 365

Tyr Asp Ala Ile Asn Gly Ser Gln Leu Tyr Ala Ile Ser Asp Ser Val
    370                 375                 380

Ala Lys Arg Leu Gly Gly Gly Ala Ala Val Asp Val Asp Asp Gly Thr
```

385 390 395 400

Val Thr Ala Pro Thr Tyr Asn Leu Lys Asn Gly Ser Lys Asn Asn Val
405 410 415

Gly Ala Ala Leu Ala Val Leu Asp Glu Asn Thr Leu Gln Trp Asp Gln
420 425 430

Thr Lys Gly Lys Tyr Ser Ala Ala His Gly Thr Ser Ser Pro Thr Ala
435 440 445

Ser Val Ile Thr Asp Val Ala Asp Gly Thr Ile Ser Ala Ser Ser Lys
450 455 460

Asp Ala Val Asn Gly Ser Gln Leu Lys Ala Thr Asn Asp Asp Val Glu
465 470 475 480

Ala Asn Thr Ala Asn Ile Ala Thr Asn Thr Ser Asn Ile Ala Thr Asn
485 490 495

Thr Ala Asn Ile Ala Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp
500 505 510

Ser Val Gly Asp Leu Gln Ala Asp Ala Leu Leu Trp Asn Glu Thr Lys
515 520 525

Lys Ala Phe Ser Ala Ala His Gly Gln Asp Thr Thr Ser Lys Ile Thr
530 535 540

Asn Val Lys Asp Ala Asp Leu Thr Ala Asp Ser Thr Asp Ala Val Asn
545 550 555 560

Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val Ala Thr Asn Thr Thr
565 570 575

Asn Ile Ala Asn Asn Thr Ser Asn Ile Ala Thr Asn Thr Thr Asn Ile
580 585 590

Ser Asn Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys
595 600 605

Trp Asp Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Thr Glu Thr
610 615 620

```
Thr Ser Lys Ile Thr Asn Val Lys Asp Gly Asp Leu Thr Thr Gly Ser
625                 630                 635                 640

Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val
                645                 650                 655

Ala Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Ser Asn
            660                 665                 670

Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys Trp Asp
        675                 680                 685

Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Asn Asn Thr Ala Ser
    690                 695                 700

Lys Ile Thr Asn Ile Leu Asp Gly Thr Val Thr Ala Thr Ser Ser Asp
705                 710                 715                 720

Ala Ile Asn Gly Ser Gln Leu Tyr Asp Leu Ser Ser Asn Ile Ala Thr
                725                 730                 735

Tyr Phe Gly Gly Asn Ala Ser Val Asn Thr Asp Gly Val Phe Thr Gly
            740                 745                 750

Pro Thr Tyr Lys Ile Gly Glu Thr Asn Tyr Tyr Asn Val Gly Asp Ala
        755                 760                 765

Leu Ala Ala Ile Asn Ser Ser Phe Ser Thr Ser Leu Gly Asp Ala Leu
    770                 775                 780

Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Thr Asn
785                 790                 795                 800

Gly Asp Ala Ser Val Ile Thr Asp Val Ala Asp Gly Glu Ile Ser Asp
                805                 810                 815

Ser Ser Ser Asp Ala Val Asn Gly Ser Gln Leu His Gly Val Ser Ser
            820                 825                 830

Tyr Val Val Asp Ala Leu Gly Gly Gly Ala Glu Val Asn Ala Asp Gly
        835                 840                 845
```

```
Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Asp Tyr Asp Asn
    850                 855                 860

Val Gly Asp Ala Leu Asn Ala Ile Asp Thr Thr Leu Asp Asp Ala Leu
865                 870                 875                 880

Leu Trp Asp Ala Asp Ala Gly Glu Asn Gly Ala Phe Ser Ala Ala His
                885                 890                 895

Gly Lys Asp Lys Thr Ala Ser Val Ile Thr Asn Val Ala Asn Gly Ala
            900                 905                 910

Ile Ser Ala Ala Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr
        915                 920                 925

Thr Asn Lys Tyr Ile Ala Asp Ala Leu Gly Gly Asp Ala Glu Val Asn
    930                 935                 940

Ala Asp Gly Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Glu
945                 950                 955                 960

Tyr Asn Asn Val Gly Asp Ala Leu Asp Ala Leu Asp Asp Asn Ala Leu
                965                 970                 975

Leu Trp Asp Glu Thr Ala Asn Gly Gly Ala Gly Ala Tyr Asn Ala Ser
            980                 985                 990

His Asp Gly Lys Ala Ser Ile Ile  Thr Asn Val Ala Asn  Gly Ser Ile
        995                 1000                1005

Ser Glu  Asp Ser Thr Asp Ala  Val Asn Gly Ser Gln  Leu Asn Ala
    1010                1015                1020

Thr Asn  Met Met Ile Glu Gln  Asn Thr Gln Ile Ile  Asn Gln Leu
    1025                1030                1035

Ala Gly  Asn Thr Asp Ala Thr  Tyr Ile Gln Glu Asn  Gly Ala Gly
    1040                1045                1050

Ile Asn  Tyr Val Arg Thr Asn  Asp Asp Gly Leu Ala  Phe Asn Asp
    1055                1060                1065
```

```
Ala Ser  Ala Gln Gly Val Gly  Ala Thr Ala Ile Gly  Tyr Asn Ser
    1070                1075                1080

Val Ala  Lys Gly Asp Ser Ser  Val Ala Ile Gly Gln  Gly Ser Tyr
    1085                1090                1095

Ser Asp  Val Asp Thr Gly Ile  Ala Leu Gly Ser Ser  Ser Val Ser
    1100                1105                1110

Ser Arg  Val Ile Ala Lys Gly  Ser Arg Asp Thr Ser  Ile Thr Glu
    1115                1120                1125

Asn Gly  Val Val Ile Gly Tyr  Asp Thr Thr Asp Gly  Glu Leu Leu
    1130                1135                1140

Gly Ala  Leu Ser Ile Gly Asp  Asp Gly Lys Tyr Arg  Gln Ile Ile
    1145                1150                1155

Asn Val  Ala Asp Gly Ser Glu  Ala His Asp Ala Val  Thr Val Arg
    1160                1165                1170

Gln Leu  Gln Asn Ala Ile Gly  Ala Val Ala Thr Thr  Pro Thr Lys
    1175                1180                1185

Tyr Phe  His Ala Asn Ser Thr  Glu Glu Asp Ser Leu  Ala Val Gly
    1190                1195                1200

Thr Asp  Ser Leu Ala Met Gly  Ala Lys Thr Ile Val  Asn Gly Asp
    1205                1210                1215

Lys Gly  Ile Gly Ile Gly Tyr  Gly Ala Tyr Val Asp  Ala Asn Ala
    1220                1225                1230

Leu Asn  Gly Ile Ala Ile Gly  Ser Asn Ala Gln Val  Ile His Val
    1235                1240                1245

Asn Ser  Ile Ala Ile Gly Asn  Gly Ser Thr Thr Thr  Arg Gly Ala
    1250                1255                1260

Gln Thr  Asn Tyr Thr Ala Tyr  Asn Met Asp Ala Pro  Gln Asn Ser
    1265                1270                1275

Val Gly  Glu Phe Ser Val Gly  Ser Ala Asp Gly Gln  Arg Gln Ile
```

```
    1280                1285                1290

Thr Asn  Val Ala Ala Gly Ser  Ala Asp Thr Asp Ala  Val Asn Val
    1295                1300                1305

Gly Gln  Leu Lys Val Thr Asp  Ala Gln Val Ser Gln  Asn Thr Gln
    1310                1315                1320

Ser Ile  Thr Asn Leu Asp Asn  Arg Val Thr Asn Leu  Asp Ser Arg
    1325                1330                1335

Val Thr  Asn Ile Glu Asn Gly  Ile Gly Asp Ile Val  Thr Thr Gly
    1340                1345                1350

Ser Thr  Lys Tyr Phe Lys Thr  Asn Thr Asp Gly Val  Asp Ala Ser
    1355                1360                1365

Ala Gln  Gly Lys Asp Ser Val  Ala Ile Gly Ser Gly  Ser Ile Ala
    1370                1375                1380

Ala Ala  Asp Asn Ser Val Ala  Leu Gly Thr Gly Ser  Val Ala Thr
    1385                1390                1395

Glu Glu  Asn Thr Ile Ser Val  Gly Ser Ser Thr Asn  Gln Arg Arg
    1400                1405                1410

Ile Thr  Asn Val Ala Ala Gly  Lys Asn Ala Thr Asp  Ala Val Asn
    1415                1420                1425

Val Ala  Gln Leu Lys Ser Ser  Glu Ala Gly Gly Val  Arg Tyr Asp
    1430
```